RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/569,076_
Source: _1 fwp_
Date Processed by STIC: _3/2/06_

ENTERED

RAW SEQUENCE LISTING   DATE: 03/02/2006
PATENT APPLICATION: US/10/569,076   TIME: 10:28:51

Input Set : A:\SEQlist003.txt
Output Set: N:\CRF4\03022006\J569076.raw

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        7 <110> APPLICANT: BERDEL, Wolfgang E.
        8         MESTERS, Rolf M.
       10 <120> TITLE OF INVENTION: Fusion polypeptides for antivascular tumor therapy
       12 <130> FILE REFERENCE: 20490.003
C-->   14 <140> CURRENT APPLICATION NUMBER: US/10/569,076
C-->   14 <141> CURRENT FILING DATE: 2006-02-21
       14 <150> PRIOR APPLICATION NUMBER: PCT/EP04/009364
       15 <151> PRIOR FILING DATE: 2004-08-20
       17 <150> PRIOR APPLICATION NUMBER: DE 10338733.1
       19 <151> PRIOR FILING DATE: 2003-08-22
       20 <160> NUMBER OF SEQ ID NOS: 41
       22 <170> SOFTWARE: PatentIn version 3.1
       25 <210> SEQ ID NO: 1
       26 <211> LENGTH: 263
       27 <212> TYPE: PRT
       28 <213> ORGANISM: Homo sapiens
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       37 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
       38             20                  25                  30
       40 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
       41         35                  40                  45
       43 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
       44     50                  55                  60
       46 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
       47 65                  70                  75                  80
       49 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
       50                 85                  90                  95
       52 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
       53             100                 105                 110
       55 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
       56         115                 120                 125
       58 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
       59     130                 135                 140
       61 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
       62 145                 150                 155                 160
       64 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
       65                 165                 170                 175
       67 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
       68             180                 185                 190
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   70 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
   71          195                 200             205
   73 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile
   74      210                 215                 220
   76 Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile
   77 225                 230                 235                 240
   79 Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu
   80              245                 250             255
   82 Asn Ser Pro Leu Asn Val Ser
   83              260
   88 <210> SEQ ID NO: 2
   89 <211> LENGTH: 218
   90 <212> TYPE: PRT
   91 <213> ORGANISM: Homo sapiens
   93 <220> FEATURE:
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   96 <400> SEQUENCE: 2
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  100 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
  101              20                  25                  30
  103 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
  104          35                  40                  45
  106 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
  107      50                  55                  60
  109 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
  110 65                  70                  75                  80
  112 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
  113              85                  90                  95
  115 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
  116              100                 105                 110
  118 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
  119          115                 120                 125
  121 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
  122      130                 135                 140
  124 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
  125 145                 150                 155                 160
  127 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
  128              165                 170                 175
  130 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
  131              180                 185                 190
  133 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
  134          195                 200                 205
  136 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg
  137      210                 215
  141 <210> SEQ ID NO: 3
  142 <211> LENGTH: 224
  143 <212> TYPE: PRT
  144 <213> ORGANISM: Artificial
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W--> 147 <221> NAME/KEY: Amino acid sequence of tTF-GRGDSP
      148 <223> OTHER INFORMATION: Synthetic construct
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      154 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
      155             20                  25                  30
      157 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
      158         35                  40                  45
      160 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
      161     50                  55                  60
      163 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
      164 65                  70                  75                  80
      166 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
      167                 85                  90                  95
      169 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
      170             100                 105                 110
      172 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
      173         115                 120                 125
      175 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
      176         130                 135                 140
      178 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
      179 145             150                 155                 160
      181 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
      182             165                 170                 175
      184 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
      185             180                 185                 190
      187 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
      188         195                 200                 205
      190 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Arg Gly Asp Ser Asp
      191     210                 215                 220
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      197 <211> LENGTH: 225
      198 <212> TYPE: PRT
      199 <213> ORGANISM: Artificial
      201 <220> FEATURE:
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      203 <223> OTHER INFORMATION: Synthetic construct
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      206 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
      207 1               5                   10                  15
      209 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
      210             20                  25                  30
      212 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
      213         35                  40                  45
      215 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
      216     50                  55                  60
      218 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
```

```
219 65                     70              75                  80
221 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
222                 85                  90                  95
224 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
225             100             105                 110
227 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
228         115                 120                 125
230 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
231     130                 135                 140
233 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
234 145                 150                 155                 160
236 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
237             165                 170                 175
239 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
240             180                 185                 190
242 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
243         195                 200                 205
245 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Asn Gly Arg Ala His
246         210                 215                 220
248 Ala
249 225
256 <210> SEQ ID NO: 5
257 <211> LENGTH: 228
258 <212> TYPE: PRT
259 <213> ORGANISM: Artificial
261 <220> FEATURE:
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W--> `262 <221> NAME/KEY: Amino acid sequence of tTF-GALNGRSHAG`

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263 <223> OTHER INFORMATION: Synthetic construct
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267 1               5                   10                  15
269 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
270             20                  25                  30
272 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
273         35                  40                  45
275 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
276     50                  55                  60
278 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
279 65                  70                  75                  80
281 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
282                 85                  90                  95
284 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
285             100                 105                 110
287 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
288         115                 120                 125
290 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
291     130                 135                 140
293 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
294 145                 150                 155                 160
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Input Set : A:\SEQlist003.txt
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296 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
297              165           170           175
299 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
300          180           185           190
302 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
303          195           200           205
305 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Ala Leu Asn Gly Arg
306     210           215           220
308 Ser His Ala Gly
309 225
314 <210> SEQ ID NO: 6
315 <211> LENGTH: 225
316 <212> TYPE: PRT
317 <213> ORGANISM: Artificial
319 <220> FEATURE:
320 <221> NAME/KEY: Amino acid sequence of tTF-GCNGRCG
321 <223> OTHER INFORMATION: Synthetic construct
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324 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
325 1             5             10            15
327 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
328          20            25            30
330 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
331          35            40            45
333 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
334     50            55            60
336 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
337 65            70            75            80
339 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
340              85            90            95
342 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
343          100           105           110
345 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
346          115           120           125
348 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
349     130           135           140
351 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
352 145           150           155           160
354 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
355              165           170           175
357 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
358          180           185           190
360 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
361          195           200           205
363 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Cys Asn Gly Arg Cys
364     210           215           220
366 Gly
367 225
374 <210> SEQ ID NO: 7
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/02/2006
PATENT APPLICATION: **US/10/569,076**   TIME: 10:28:52

Input Set : **A:\SEQlist003.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,10,11,12,13,14,15,18,19,20,21,22,23,24,25,26,27,28,29,30,31
Seq#:32,33,34,35,36,37,38,39,40,41

VERIFICATION SUMMARY   DATE: 03/02/2006
PATENT APPLICATION: **US/10/569,076**   TIME: 10:28:52

Input Set : **A:\SEQlist003.txt**
Output Set: **N:\CRF4\03022006\J569076.raw**

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:94 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:202 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:262 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:320 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:380 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:440 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:498 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:501 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:536 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:572 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:609 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:646 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:681 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:716 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:749 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:751 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:762 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:765 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:779 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:807 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:820 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:834 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
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L:953 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:973 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:1036 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:1141 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:1156 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:1172 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
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